

This Page Is Inserted by IFW Operations
and is not a part of the Official Record

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images may include (but are not limited to):

- BLACK BORDERS
- TEXT CUT OFF AT TOP, BOTTOM OR SIDES
- FADED TEXT
- ILLEGIBLE TEXT
- SKEWED/SLANTED IMAGES
- COLORED PHOTOS
- BLACK OR VERY BLACK AND WHITE DARK PHOTOS
- GRAY SCALE DOCUMENTS

IMAGES ARE BEST AVAILABLE COPY.

**As rescanning documents *will not* correct images,
please do not report the images to the
Image Problem Mailbox.**

**ARABIDOPSIS THALIANA FAE1 PROMOTER:
(LENGTH 934 bp)**

-950	ACTCA	TAAAAA	<u>CTAG</u>	<u>TAGATTGGTT</u>	<u>GGTTGGTTTC</u>	<u>CATGTACCA</u>
				Atp_{ro}FW	→	
-900	AAGGCTTACC	CTATTAGTTG	AAAGTTGAAA	CTTTGTTCCC	TACTCAATTC	
-850	CTAGTTGTGT	AAATGTATGT	ATATGTAATG	CGTATAAAAC	GTAGTACTTA	
-800	AATGACTAGG	AGTGGTTCTT	GAGACCGATG	AGAGATGGGA	GCAGAACTAA	
-750	AGATGATGAC	ATAATTAAGA	ACGAATTTGA	AAGGCTCTTA	GGTTTGAATC	
-700	CTATTCGAGA	ATGTTTTTGT	CAAAGATAGT	GGCGATTTTG	AACCAAAGAA	
-650	AACATTTAAA	AAATCAGTAT	CCGGTTACGT	TCATGCAAAT	AGAAAGTGGT	
-600	CTAGGATCTG	ATTGTAATTT	TAGACTTAAA	GAGTCTCTTA	AGATTCAATC	
-550	CTGGCTGTGT	ACAAAAC	TAC	AAATAATATA	TTTTAGACTA	TTTGGCCTTA
-500	ACTAAACTTC	CACTCATTAT	TTACTGAGGT	TAGAGAATAG	ACTTGCGAAT	
-450	AAACACATTC	CCGAGAAATA	CTCATGATCC	CATAATTAGT	CAGAGGGTAT	
-400	GCCAATCAGA	TCTAAGAACA	CACATTCCCT	CAAATTTTAA	TGCACATGTA	
-350	ATCATAGTTT	AGCACAATTC	AAAAATAATG	TAGTATTAAA	GACAGAAATT	
-300	TGTAGACTTT	TTTTTTGGCGT	TAAAGGAAGA	CTAAGTTTAT	ACGTACATTT	
-250	TATTTTAAAGT	GGAAAACCGA	AATTTTCCAT	CGAAATATAT	GAATTTAGTA	
-200	TATATATTTT	TGCAATGTAC	TATTTTGCTA	TTTTGGCAAC	TTTCAGTGGA	
-150	CTACTACTTT	ATTACAATGT	GTATGGATGC	ATGAGTTTGA	GTATACACAT	
-100	GTCTAAATGC	ATGCTTTGCA	AAACGTAACG	GACCACAAAA	GAGGATCCAT	
-50	GCAAATACAT	CTCATAGCTT	CCTCCATTAT	<u>TTTCCGACAC</u>	<u>AAACAGAGCA</u>	
				← Atp_{ro}RV		
1	ATG	ACGTCCG	TTAACGTTAA	GCTCCTT		

FIG. 1

FIG. 2A

```

-450 GTTACATAGA TTTGGAAACA CTTCATCTAG CTCAATATGG TATGAGTTGG
-400 CATACATAGA AGCAAAAGGA AGGATGAAGA AAGGTAATAA AGTTTGGCAG
-350 ATTGCTTTAG GGTCAAGGCTT TAAGTGTAAC AGTGCAGTTT GGGTGGCTCT
-300 AAACAATGTC AAAGCTTCGA CAAATAGTCC TTGGGAACAC TGCATCGACA
-250 GATACCCGGT CAAAATTGAT TCTGATTCAG GTAAGTCAGA GACTCGTGTC
-200 CAAAACGGTC GGTCCTAATA AACGATGTTT GCTCTCTTTC GTTTCTTTTT
-150 ATTTGTTATA ATAATTTGAT GGCTACGATG TTTCTCTTGT TTGTTATGAA
-100 TAAAGAATGC AATGGTGTTT TAGTATTTGA TTGTTTTACA TGTATGTATC
-50 TCTTATTTAC ATGAAATTTT TAAACGCCTA AAAAAAAAAA CGGAATTCGG
      ← BnproRV
1  ATGACGTCCA TTAACGTAAA GCTCCTTTAC CATTACGTCA TAACCAACCT
51 TTTCAACCTT TGCTTCTTTC CGTTAACGGC GATCGTCGCC GGAAAAGCCT
      ← Bnwalk2
101 ATCGGCTTAC CATAGACGAT CTTCAACCACT TATACTATTC CTATCTCCAA
151 CACAACCTCA TAACCATCGC TCCACTCTTT GCCTTCACCG
      ← Bnwalk1

```



4/15

LUNARIA ANNUA FAE1 PROMOTER:
(LENGTH 1069 bp)

+
-1100 CG CCGGGGAGTT TCAGCTTAAC CGGTAAAATT
LaproFW →
-1050 GGCCTGTACA TATATTTACC ACTGAGTAAA GACATCAGTT AATGATTTGT
-1000 TGTTACTCAA TTGGGCTAAG TGTATTATTA TATGTGTTGT ATATAATAAA
-950 GGTAGAACGT AAATTTACTA AGAATGTGTT TTTCCAATGT GATTGCTCTT
-900 TGGCCTCTTA GGTTTGAATC CTACTCGAGA AGACTAATTT TAATTTACTG
-850 GCAAAAATAG AAATCAATTT ATAAGTGTTT AAACAAATCG ATGGTATAAC
-800 TGATTAGTGA TCACTCTTAG GTTTTGATCC AACTCGAGTA TTGAGTATTG
-750 AACGCTTTTT TTAAATAAAA TCTTGATTTT TAAATTGGTT TTTTGAGTAA
-700 AAAAGTTCTT AATATTTTCT CTTTGTTTTA ATGGGTTTGT TTTGCATTTT
-650 ATAAGCTTAA TTTTCTAAT TTAATATTTT ATCTATCATC GTCCGTAAAG
-600 TTTTATTTGG CACAACTTG TTTTACTTTT CTACCTTATA ATTTGGGAAC
-550 TGGTTGAGTC AAAGCGTACC GGACAAATAT GTTTTATATT CTTATTTAAG
-500 AATTAACACT CATCTCATAA TTAGTCAGAG GCTAGGGAGA TTCAGCCAAT
-450 CAATGCTAAC AACAAAATTC TCTTAATGAT CTAACGATGC TATTTAATAT
-400 TCGGATCAGT ATTCTTAAAT AAGAATATAA AACTAATTCA ATAGTTACAG
-350 ATAAAACTT ATATAGACTT TTTTATTTGG AATATAAAAG TATCAATATA
-300 TTATAGACAA TATTTATAAC GTTAAAAATA CAATATTTAT ATTTTTTATA
-250 TATTTATTTT AAATTGAAAA GCATTACTTC TATCGAAATG AATTTTAGTA
-200 TATTAATTAA TATTTTTTTT ATCGGACTAC TTTCTATTT TGGCACCTTT
-150 CATCTGACTA CTAATTTATT TCAATGTGTA TGCATGCATG AGCATGAGTA

FIG. 3A

```

-100 ATACACATGT CTATATAAAT GCATGTAAAA CGTAACGGAC CACAAAAGTG
-50 GATCCATACA AATACATCTC ATCGCACCCCT CTCCGACACA AAACTGAACA
                                     ← LaproRV
  1  ATGACGTCTG TGAACGTAAA ACTCCTTTAC CATTACGTCA TAACCAACTT
51  TTTCAACCTC TGTTTCTTCC CACTGACGGG GATCCTCGCC GGAAAAGGCT
                                     ← Lawalk2
101 CTCGTCTTAC CACAAACGAT CTCCACCA
                                     ← Lawalk1

```

FIG. 3B

ALIGNMENT OF *A.t.*, *L.a.* AND *B.n.* *FAE1* PROMOTERS

FIG. 4A

+



7/15

ALIGNMENT OF *A.t.*, *L.a.* AND *B.n.* *FAE1* PROMOTERS (CONTINUED)

<i>A.t.</i>	TTGGTTTCCA--TGTACCAGAAGGCTTACCCTAT-TAGTTGAAAGTTGAAACTTTGTTC
<i>L.a.</i>	TTGTTACTCAATTGGGCTAAGTGTATTATTATAT-GTGTGTATATAATAAAGGTAGAAC
<i>B.n.</i>	ACTTGTTCATGTCCATAAAATACGTATGCTCTTGTGGTGAGCACAGAGAACATCACTT
	** * ** * * * * *
Con. 4	WYKKKWYBCANNTSBRYHARRWKDMKTAYBMTMTNKWGKTGWRHRYWRWRAMBDTVDHYY
<i>A.t.</i>	CTACTCAATTCCTAGTTGTGTAAATGT---ATGTATATGTAAT---GCGTATAAAACGTA
<i>L.a.</i>	GTAA--ATTTACTAAGAATGTGTTTTTCCAATGTGATTGCTCTTTGGCCTCTTAGGTTTG
<i>B.n.</i>	ATAA-CATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAAATTGCTTGTTCCTGTT
	* * * * * * * * * *
Con. 4	VTAMNNAWTTMCMMDKDDKRTRWWKKNNNATGWDDDTKYHMWNNNGCBTVTWMVRYKTD
<i>A.t.</i>	GTACTTAAATGACTAGGAGTGGTCTTGAGACCGATGAGAGATGGGAG-CAGAACTAAAG
<i>L.a.</i>	AATCCTACTCGAGAAG-ACTAATTTTAAATTTACTGGCAAAAATAGAAA-TCAATTTATAA
<i>B.n.</i>	GGTGGGGC-CGCTATTTTGCTCTCCAACAAGCCTGGAGATCGTAGACGGTCCAAGTACGA
	* * * * *
Con. 4	RDWSBKRMNYGMBWKNWSYDVITYYWWDDMCKRKVRRWVRTRGRMRNYMVAWBTahrR
<i>A.t.</i>	AT--GATGACATAATTA-----AGAACGAATTTGA-AAGG-CTCTTAGGTTTGAATCCT
<i>L.a.</i>	GT--GTTTAAACAAATCGATGGTATAACTGATTAGT-GATCACTCTTAGGTTTGTATCCA
<i>B.n.</i>	GCTAGTTTCACACGGTTTCAACGCATACCGGAGCTGACGACAAGTCTTTTCGTTGCGTGCA
	* * * * * * * * * * * * *
Con. 4	RYNNGWTBAMAYRRWTMNNNNNNNAKAMCKRAKYWGNRABVNSTCTTWKSKTTKVRTSCH
<i>A.t.</i>	ATTCGAGAATGTTTTTGTCAAAGATAGTGGCGATTTTGAACCAAAGAAAACATTTAAA-A
<i>L.a.</i>	ACTCGAGTATTGAGTATTGAACGCTT-----TTTTTAAATAAAATCTTGATTTTTTA-A
<i>B.n.</i>	A--CAAGGA-GACGATGAGAACGGCAA-----AATCGGAGTGAGTTTGTCCAAGGACATA
	* * * * * * * * * * * * *
Con. 4	ANNCRAGDANKDHKWWKWSAAMGVYWNNNNNNNWYTKKARHBARWDWVHSAWKKWHANA
<i>A.t.</i>	AATCAGTATCCGGTTAC----GTTTCATGCAAATAGAAAGTGGTCTA---GGATCTGATT-
<i>L.a.</i>	ATTGGTTTTTTGAGTAAAAAAGTTCTTAATATTTCTCTTTGTTTTAATGGGTTTGTTT-
<i>B.n.</i>	ACCGATGTTGCTGGTCAACGGTTAAGAAAAACATAGCAACGTT-----GGGTCCGTTGA
	* * * * * * * * * * *
Con. 4	AHYSRKKWTBYKRKTMVNNNNGTTMWKRMWAWYWKMDMDWBGTYNNNNNGGRTYYGWTKN
<i>A.t.</i>	GTAATTTTAGA--CTTAAAGAGTCTC--TTAAGATTCAATCCTGGCT-GTGTACAAAAC
<i>L.a.</i>	TGCATTTTATAAGCTTAATTTTTCTAATTTAATATTTTATCTATCATCGTCCGTAAAGTT
<i>B.n.</i>	TTCTTCCGTTAAGCGAGAAACTTCTT--TTTTTCGTTA--CCTTCATGGGCAAGAAACTT
	* * * * * * * * * * * * *
Con. 4	KKMWTYYKWKANCKWRAWDHKTCTHNNTTWWMKTYWNNCYWKSMTNGKSHRBAAAVYT
<i>A.t.</i>	ACAAATAATATA----TTTAGACTATTTGGCCTTAACTAAACTTCCA-CTCATTATTTA
<i>L.a.</i>	TTATTTGGCACAAACTTGTTTTACTTTTCTACCTTA--TAATTTGGGAAGTGGTGGAGT-
<i>B.n.</i>	TTCAAAGATAAAATCAACATTACTACGTCCCGGATTTCAAACTTGCTATTGACCATTTT
	* * * * * * * * * * * * *
Con. 4	WYMWWRRYAHANNNNWDYWWKACTWYKYBVCSKWNNYAAYWTKSSWNYTSRYRWKTN
<i>A.t.</i>	-CTGAGGTTAGAGAA--TAGACTTGCGAATAAACACATTCCCGAGAAATACTCATGATCC
<i>L.a.</i>	-CAAAGCGTACCGGA--CAAATATGTTT-TATATTCTTATTTAAGAATTAACACTCATCT
<i>B.n.</i>	TGTATACATGCCGGAGGCAGAGCCGTGATTGATGTGCTAGAGAAGAACCAGCCCTAGCA
	* * * * * * * * * * * * *
Con. 4	NSWRWRS DTRSMGRANNYARABHYGYKWNTRWWBWSHTWBHBRAGAAHYWMBMMYBAKCH

FIG. 4B



8/15

ALIGNMENT OF *A.t.*, *L.a.* AND *B.n.* *FAE1* PROMOTERS (CONTINUED)

CE3

A.t. CATAATTAGTCAGAGGGTATG-----CCAATCAGATCTAAGAAACACATTCCCTC
L.a. CATAATTAGTCAGAGGCTAGGGAGATTAGCCAATCAATGCTAACACAAA-ATTCTCTT
B.n. CCGATCGATGTAGAGGC-----ATCAAGATCAACGTTACATAGATTGG

* *

Con. 4 CMKAWYKAKKYAGAGGSNNNNNNNNNNNNNNNNNNNNATCARDYYAASRWYAMANAKWYYYKB

A.t. AA--ATTTTA--ATGCAC-ATGTAATCAT-----AGTTT-----AGCACAAATTCAAAA
L.a. AATGATCTAACGATGCT--ATTTAATATTCCGGATCAGTATTCTTAAATAAGAATATAAAA
B.n. AAACACTTCATCTAGCTCAATATGGTATG-----AGTTGGCATACAT-AGAAG-CAAAA

* *

Con. 4 AANNAYYTHANNWGCWNNATDTRRTMWKNNNNNNNAGTWKNNNNNNNAKNASAAKNYAAAA

A.t. ATAATGTAGTA-TTAAAGACAGAAATTTGTA--GACTTTTTT---TTGGCGT-TAAAGG
L.a. CTAATTCATAGTTACAGATAAAAACCTTATATAGACTTTTTTAT--TTGGAATATAAAAG
B.n. GGAAGGATGAA-GAAAGGTAATAAAGTTTGGCAGATTGCTTTAGGGTCAGGCTTTAAGTG

* *

Con. 4 VKAAKKHWRWANKWAMRGWHADAAABTTDKRNGAYTKYTTNNNNNTYRGVVTNTAARDG

A.t. AA-----GACTAAGTTTATA-CGT-----ACATTT-TATTTTAAGT
L.a. TATCAATATATTATA-GACAATATTTATAACGTTAAAAATACAATATTTTATTTTAT
B.n. TAACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAAGCTTCGACAAATAGTCTTGGGA

* *

Con. 4 WANNNNNNNNNNNNNGWSDMWVTWVAYANYGTNNNNNNNNNNAYAWWTNKWYYTTDDRW

CE1

A.t. GGA-----AAACCGAAATT--TCCATCGAAATATATGA--ATTT-AGTATAT---
L.a. ATATTTATTTCAAATTGAAAGCATTACTTCTATCGAAATGA--ATTTTAGTATATTAAT
B.n. ACACT-----GCATCGACAGATACCCGGTCAAATGATTCTGATTCTAGGTAAGTCAGA

* *

Con. 4 RBAYTNNNNNNRMAYYGAYADDYAYYMSDTCDAWMKWDATKMNNATTYNRGTAWRNTNNNN

G-box2

A.t. --ATATTTCTGCAAT-----GTACTATTTTGCTATTTTGGCAA-CTTTCAGTGGACTAC
L.a. TAATATTTTAAATC-----GGACTACTTTCTATTTTGGCAC-CTTTCATCTGACTAC
B.n. GACTCGTGTCACAAACGGTCCGTCTAATAAACGATGTTTGGTCTCTTTCTGTTT--CTTT

* *

Con. 4 NNMTMKTKYBHAAWNNNNNNGKMCTAHTWWVCKATKTTKGCWMNCTTTCRKYKNNCTWY

G-box1

A.t. TACTTTATTACAATGTGT--ATGGATGC-ATGAG---TTTGAGTA-TACACATGCTAAA
L.a. TAATTTATTTCAATGTGT--ATGCATGC-ATGAG---CATGAGTAATACACATGCTATA
B.n. TTATTTGTTATAATAATTGATGGCTACGATGTTTCTCTGTTTGTATGAATAAGAAT

* *

Con. 4 TWMTTTRTTWYAATRWKTNNATGSMTRCNATGWKNNNYWTGWKTRWTAYRMATRWKAWW

A-300 EM1 ABA

A.t. TGCATGCT-TTGCAAAACGTAACGGACC-ACAAAAGAGGATCCAATGCAAAATACATCTCAT
L.a. TAAATGCA-T-GTAAAACGTAACGGACC-ACAAAAGTGGATCCATACAAATACATCTCAT
B.n. GCAATGGTGTCTAGTATTTGATTGTTTTACATGTATGTATCTCTT-ATTTACATGAAAT

* *

Con. 4 KVMATGSWNTNSYARWAYKTRAYKGWYNNACAWRWRWGKATCYMTDNAWWTACATSWMAT

A.t. AGC-TTCCTCCATTATTTTCCGACACAAA-CAGAGCA---
L.a. CGC-ACCCTC-----TCCGACACAAAACCTGAACA---
B.n. TTTTAAACGCC-----TAAAAAAGGAAACGGAATTCCG

* *

Con. 4 HKYNWHMCKCNNNNNNNNNTMMRAMAMAAANCDGARYWNNN

FIG. 4C



9/15

ALIGNMENT OF *A.t.* AND *L.a.* *FAE1* PROMOTERS
 CLUSTAL W (1.74) MULTIPLE SEQUENCE ALIGNMENT

```

A.t. -----ACTCATAA
L.a. CGCCGGGGAGTTTCAGCTTAACCGGTAAATTGGCCTGTACATATATTTACCACTGAGTA
Con.5 ACTSAKWA

A.t. AACTAGTAGAT--TGGTTGGTTGGTTTCCA--TGTACCAGAAGGCTTACCCTATTAGTT
L.a. AAGACATCAGTTAATGATTTGTTGTTACTCAATTGGGCTAAGTGATATTATATATGTGTT
Con.5 AARMYAKYAGWTNNTGRTTKGTTGKTWYYCANNTGKRCYARRWGKMTTAYYMTATKWGTT

A.t. GAAAGTTGAAACTTTGTTCCCTACTCAATTCCTAGTTGTGTAAATGT---ATGTATATGT
L.a. GTATATAATAAAGGTAGAACGTAA--ATTACTAAGAATGTGTTTTTCCAATGTGATTGC
Con.5 GWAWRTWRWAAMKKTRKWMCMSTAMNNAWTTMCTARKWRTGTRWWTKTNNNATGTRWWTGY

A.t. AAT---GCGTATAAAACGTAGTACTTAAATGACTAGGAGTGGTTCTTGAGACCGATGAGA
L.a. TCTTTGGCCTCTTAGGTTTGAATCCTACTCGAGAAG-ACTAATTTTAATTTACTGGCAA
Con.5 WMTNNNGCSTMTWARRYKTRRWWCYTAMWYGASWAGNASTRTTYTWRWKWCKRKSARA

A.t. GATGGGAGCAGAACTAAAGATGATGACATAATTA-----AGAACGAATTTGAAAGG-CT
L.a. AATAGAAATCAATTTATAAGTGTTTAAACAAATCGATGGTATAACTGATTAGTGATCACT
Con.5 RATRGRARYMRAWYTAWARRTGWTAMAYAAWTMNNNNNNAKAACKRATTWGWRAKSNT

A.t. CTTAGGTTTGAATCCTATTCGAGAATGTTTTTGTCAAAGATAGTGGCGATTTTGAACCAA
L.a. CTTAGGTTTGTATCCAACCTCGAGTATTGAGTATTGAACGCTT-----TTTTTAAATAA
Con.5 CTTAGGTTTKRATCCWAYTCGAGWATKKWKTWKTSAAMGMTWNNNNNNNTTTTKAAMYAA

A.t. AGAAAACATTTAAAAATCAGTATCCGGTTAC---GTTTCATGCAAATAGAAAGTGGTCT
L.a. AATCTTGATTTTAAATTTGGTTTGTGAGTAAAAAAGTTCTTAATATTTTCTCTTTGTTT
Con.5 ARWMWSATTTWAAAWTSRKWTYTYGRKTAMNNNNGTTCTWTRMWAWTWKWMKTKGTTT

A.t. A---GGATCTGATTGTAATTTTAGA--CTTAAAGAGTCTC--TTAAGATTCAATCCTGGC
L.a. TAATGGGTTTGTTTGCAATTTATAAGCTTAATTTCTTAATTTAATATTTATCTATCA
Con.5 WNNNGGRITYTGWTTKKMATTTTAKANNCTTAAWKWKCTMNNNTTAAKATTYWATCYWKS

A.t. T-GTGTAACAACTACAAATAATATA----TTTAGACTATTTGGCCTTAACCTAACTTC
L.a. TCGTCCGTAAAGTTTATTTGGCACAACTTGTTTTACTTTTCTACCTTA--TAATTTGG
Con.5 TNGTSYRYAAARYTWYAWWTRRYAYANNNTKTWKACTIONWTTKYRCCTANNTAAWYTKS

A.t. CA-CTCATTATTTACTGAGGTTAGAGAATAGACTTGCGAATAAACACATTCCCAGAAAT
L.a. GAACTGGTTGAGT-CAAAGCGTACGGGACAAATATGTTT-TATATTCTTATTTAAGAATT
Con.5 SANCTSRTRWKTNCWRAGSKTASMGRAAYARAYWTGYKWNTAWAYWCWWTWYRAGAAWT

A.t. -432 ACTCATGATCCCATAATTAGTCAGAGGGTATG-----CAATCAGATCTAAGAACA
L.a. AACACTCATCTCATAATTAGTCAGAGGGCTAGGGAGATTGAGCCAATCAATGCTAACAACA
Con.5 AMYMTSATCYCATAATTAGTCAGAGGSTAKGNNNNNNNNNCCAATCARWKCTAASAACA
  
```

FIG. 5A



10/15

ALIGNMENT OF *A.t.* AND *L.a.* *FAE1* PROMOTERS (CONTINUED)

<i>A.t.</i>	-381	CACATTCCCTCAA--ATTTTA--ATGCACATGTAATCAT-----AGTTT-----AGCA
<i>L.a.</i>		AA-ATTCTCTTAATGATCTAACGATGCT-ATTTAATATTCGGATCAGTATCTTAAATAA * * * * *
Con.5		MANATTCTCYCTYAANNATYTWANNATGCWNATKTAATMWTNNNNNNAGTWTNNNNNNNAKMA
<i>A.t.</i>	-337	CAATTCAAAAATAATGTAGTA-TTAAAGACAGAAATTTGTA--GACTTTTTT--TTGGCG
<i>L.a.</i>		GAATATAAAACTAATTCAATAGTTACAGATAAAACTTATATAGACTTTTTTATTTGGAA * * * * *
Con.5		SAATWYAAAAMTAATKYARTANTTAMAGAYARAAAYTTRTANNGACTTTTTTNNTTGGMR
<i>A.t.</i>	-282	T-TAAAGGAA-----GACTAAGTTTATA-CGT-----ACATTT-TAT
<i>L.a.</i>		TATAAAAGTATCAATATATTATAGACAATATTTATAACGTTAAAAATACAATATTTATAT * * * * *
Con.5		TNTAAARGWANNNNNNNNNNNNNGACWAWRTTATANCGTNNNNNNNNNNAYATTTNTAT
<i>A.t.</i>	-247	TTTAAGTGGA-----AAACCGAAATT--TTCCATCGAAATATATGAATTT-AGTATA
<i>L.a.</i>		TTTTTATATATTTTATTTCAAAATTGAAAAGCATTACTTCTATCGAAATGAATTTTAGTATA * * * * *
Con.5		TTTWWRTRKANNNNNNNNNNAAYYGAAAWKNNTTMCWTCKAWMKAWATGAATTTNAGTATA
<i>A.t.</i>	-198	T-----ATATTTCTGCAAT-GTACTATTTTGCTATTTTGGCAACTTTTCACTGGGACTACT
<i>L.a.</i>		TTAATTAATATTTTTTTAATCGGACTACTTTCTTATTTTGGCACCTTTTCTCTGACTACT * * * * *
Con.5		TNNNNNNATATTTYTKYAATNGKACTAYTTTTSCTATTTTGGCAMCTTTTCAKYKGACTACT
<i>A.t.</i>	-145	ACTTTATTACAATGTGTATGGATGCATGAGTTTGAGTA-TACACATGTCTAAATGCATGC
<i>L.a.</i>		AATTTATTTCAATGTGTATGCATGCATGAGCATGAGTAATACACATGTCTATATAAATGC * * * * *
Con.5		AMTTTATTWCAATGTGTATGSATGCATGAGYWTGAGTANTACACATGTCTAWATRMATGC
<i>A.t.</i>	-86	TTTGCAAAACGTAACGGACCACAAAAGAGGATCCATGCAAATACATCTCATAGCTTCCTC
<i>L.a.</i>		AT-GTAAACGTAACGGACCACAAAAGTGGATCCATACAAATACATCTCATCGCACCTC * * * * *
Con.5		WTNGYAAAACGTAACGGACCACAAAAGNGGATCCATRCAAATACATCTCATMGWCYCCTC
<i>A.t.</i>	-26	CATTATTTTCCGACACAAA-CAGAGCA
<i>L.a.</i>		-----TCCGACACAAAAGTGAACA * * * * *
Con.5		NNNNNNNTCCGACACAAANCWGARCA

FIG. 5B



11/15

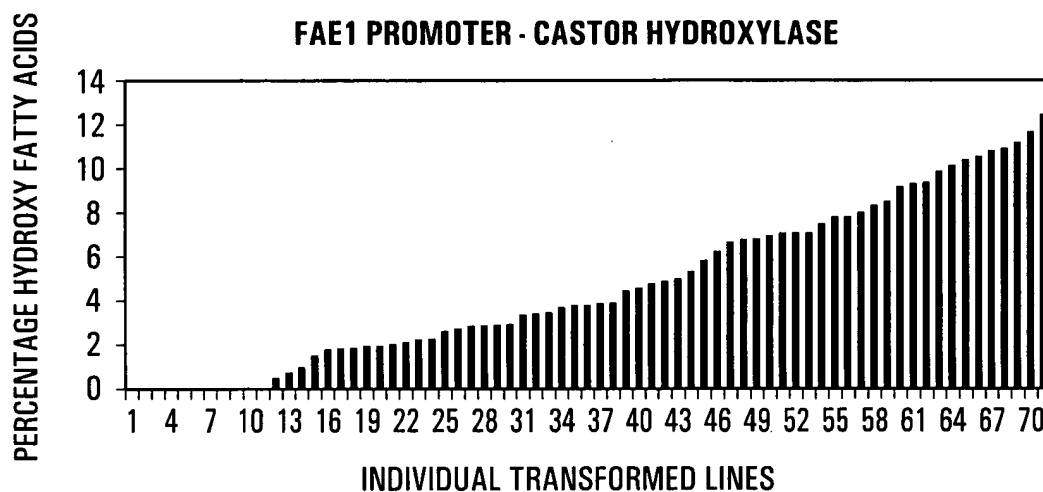


FIG. 6A

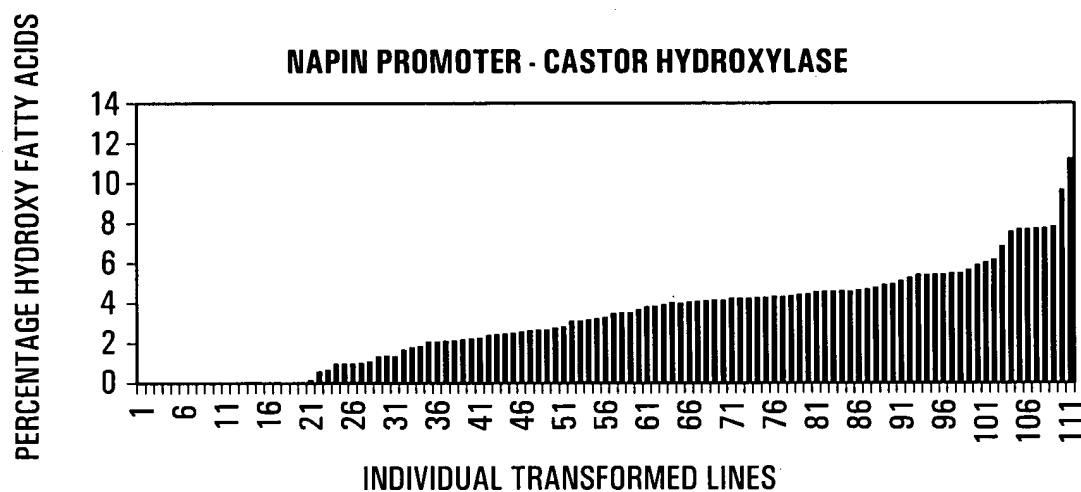


FIG. 6B



12/15

Alignment of B.n. and L.a. FAE1 promoters
 CLUSTAL W (1.81) multiple sequence alignment

```

BnFAE1  GGTGGGCAAACTCTGACTTCACCAAGAAACAACCTCGAGTCGTTATCCATCTCCTCATAA 60
LaFAE1  -----

BnFAE1  CCATCGCTCCACTCTTTGCCTTCACCGTTTTTCGGTTCGGTTCTCTACATCGCAACCCGGC 120
LaFAE1  -----

BnFAE1  CCAAACCGGTTTACCTCGTTGAGTACTCATGCTACCTTCCACCAACGCATTGTAGATCAA 180
LaFAE1  -----CGCCGGGGAGT-TTCAGCTTAACCGGTAAATTGGCCTGTACATATA 46
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  GTATCTCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAAGCTGATCCTTCTCGGAACG 240
LaFAE1  TTTACCACTGAGT-AAAGACATCAGTTAATGATT-----GTTGTTACTCAATTGGGCT 99
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  GCACGTGCGATGACTCGTCGTGGCTTGACTTCTTGAGGAAGATTCAAGAACGTTTCAGGTC 300
LaFAE1  AAGTGATTATTATATATGTTG-----TATATAATAAAGGT---AGAACGT--AAATT 147
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  TAGGCGATGAACTCACGGGCCCCGAGGGGCTGCTTCAGGTCCCTCCCCGGAAGACTTTTG 360
LaFAE1  TA--CTAAGAAATGTGTTTTTCCAATGTGATTGCTCTTTGGCCTCTTAGGTTTGAATCCTA 205
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  CGCGCGCGCGTGAAGAGACGGAGCAAGTTATCATTGGTGGCTAGAAAATCTATTCAAGA 420
LaFAE1  CT-----CGAGAAGACTAATTTTAAAT-TTACTGGCAAAAATAGAAATCAATTATATA 256
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  ACACCAACGTTAACCCTAAGATATAGGTATACTTGTGGTGAACCTCAAGCATGTTTAATC 480
LaFAE1  GTGTTTAAACAAATC--GATGGTATAACTG-ATTAGTGATCACTCTTAGGTT--TTGATC 311
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  CAACTCCATCGCTCTCCGCGATGGTCGTTAACACTTTCAAGCTCCGAAGCAACGTAAGAA 540
LaFAE1  CAACTCGAGTATTG-----AGTATTGAACGCTT-----TTTTAAATAAAATCTTGA 358
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  GCTTTAACCTTGGTGGCATGGGTTGTAGTGCCGGCGTTATAGCCATTGATCTAGCAAAGG 600
LaFAE1  TTTTAA--TTGGTTTTTTGAGTAAAAAAGTCTTAATATTTCTCTT-TGTTTTAATGG 416
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  ACTTGTTGCATGTCC-ATAAAAATACSTATGCTCTTGTGGTGAGCAGAGAAACATCACT 659
LaFAE1  GTTTGTTTTGCATTTTATAAGCTTAATTTTCTAATTTAAT-ATTTTATCTATCATCGTC 475
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  TATAACATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAAATTGCTTGTTCCTGTT 719
LaFAE1  CGTAAAGTTT-----TATTTGSCACAACTTGTTTTA---CTTTCTACCTTATA 522
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  GTGGGGCCGCTATTTTGCTCTCCAACAAGCCTGGAGATCGTAGACGGTCCAAGTACGAG 779
LaFAE1  ATTTGGGA-ACTGGTTGAGTCA-----AAGCGTACCGGACAAATATGTTTATATTC--- 573
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  CTAGTTCACACGGTTCGAACGCATACCGGAGCTGACGACAAGTCTTTTCGTTGCGTGCAA 839
LaFAE1  -TTATTTA-AGAATTAACACTCATCTCATAATTAGTCAGAGGC-----TAGGGAGATT 624
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

BnFAE1  CAAGGAGACGATGAGAACGGCAAAATCGSAGTGAGTTTSTCCAAGGACATAACCGATGTT 899
LaFAE1  CAGCCAATCAATGCTAACACAAATTTCTTTAA--TGATCTAACGATGCTATTTAATAT 682
      *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
  
```

FIG. 7A



13/15

Alignment of *B.n.* and *L.a.* *FAE1* promoters

BnFAE1	GCTGGTCTGAACGGTTAAGAAAAACATAGCAACGTTGGGTCCGTTGATTCTTCCGTTA-AG	958
LaFAE1	TCGGATCAGTATTCTTAAATAAGAATATAAA-----ACTAATTCAATAGTTACAG	732
	* * * * *	
BnFAE1	CGAGAAACTTCTTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAAGATAAAATCAA	1018
LaFAE1	ATAAAACTTATATAGACTTTTTTATTG-GAATATAAAAGTATCAATATATTATAGACA	791
	* * * * *	
BnFAE1	ACATTACTACGTCCCGGATTTCAAACTTGTATTGACCATTTTTGTATACATGCCGGAGG	1078
LaFAE1	ATATTTATA-----ACGTTAAAAATACAATATTTATATTTTTATATATTTATTCAA	845
	* * * * *	
BnFAE1	CAGAGCCGTGATTGATGTGCTAGAGAAGAACCTAGCCCTAGCACCGATCGATGTAGAGGC	1138
LaFAE1	TTGAAAAGCATTACTTCTATCGAAATGAATTTTAGT----ATATTAATTAATATTTT	901
	* * * * *	
BnFAE1	ATCAAGATCAACGTTACATAGATTTGGAACACTTCATCTAGCTCAATATGGTATGAGTT	1198
LaFAE1	AATCGGACTACTTTCTCTAT----TTTGGCACCTTTTCATCTGACT-----ACT	944
	* * * * *	
BnFAE1	GGCATACATAGAAGCAAAAGGAAGGATGAAGAAAGGTAATAAAGTTTGGCAGATTGCTTT	1258
LaFAE1	AATTATTTCAATGTGTATGCATGCATGAGCATGAGTAATA-----CACATGCTCTAT	996
	* * * * *	
BnFAE1	AGGGTCAGGCTTTAAGTGTACAGTGCAGTTTGGGTGGCTCTAAACAATGTCAAAGCTTC	1318
LaFAE1	ATAAATGCATGTAAACGTAACGG-ACCACAAAGTGGATCCATACAAATACATCTCATC	1055
	* * * * *	
BnFAE1	GACAAATAGTCCTTGGGAACACTGCATCGACAGATACCCGGTCAAATTTGATTCTGATTC	1378
LaFAE1	G-CACCCCTCTCCGACACAAACTGAACA-----	1082
	* * * * *	
BnFAE1	AGGTAAGTCAGAGACTCGTGTCCAAAACGGTCCGTCTAATAAACGATGTTTGCTCTCTT	1438
LaFAE1	-----	
BnFAE1	TCGTTTCTTTTATTGTTATAATAATTGATGGCTACGATGTTTCTCTGTTTGTTATG	1498
LaFAE1	-----	
BnFAE1	AATAAAGAAATGCAATGGTGTCTAGTATTGATTGTTTACATGTATGTATCTCTTATT	1558
LaFAE1	-----	
BnFAE1	ACATGAAATTTTAAACGCCTAAAAAACAACGGAATTCCG	1600
LaFAE1	-----	

FIG. 7B



14/15

ALIGNMENT OF *B.n.* AND *A.t.* *FAE1* PROMOTERS
 CLUSTAL W (1.81) MULTIPLE SEQUENCE ALIGNMENT

```

AtFAE1 -----
BnFAE1 GGT TGGGCAAATCTGACTTCACCAAAGAAACAACCTCGAGTCGTTATCCATCTCCTCATAA 60

AtFAE1 -----
BnFAE1 CCATCGCTCCACTCTTTGCCTTCACCGTTTTCGGTTGGGTTCTCTACATCGCAACCCGGC 120

AtFAE1 -----
BnFAE1 CCAAACCGGTTTACCTCGTTGAGTACTCATGCTACCTTCCACCAACGCATTGTAGATCAA 180

AtFAE1 -----ACTCATAAA 10
BnFAE1 GTATCTCCAAGGTCATGGATATCTTTTATCAAGTAAGAAAAGCTGATCCTTCTCGGAACG 240
          *** **

AtFAE1 ACTAGTAGATTGGTTGGT--TGGTTTCCATGTACCAGAAGGCTT-----ACCCTATTAGT 63
BnFAE1 GCACGTGCGATGACTCGTCGTGSGTTGACTTCTTGAGGAAGATTCAAGAACGTCAGGTC 300
  *  **   *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 TGAAAGTTGAACTT-TGTTCCCTACT--CAATTCCTAGTTGTGTAAATGTATGTATATG 120
BnFAE1 TAGGCGATGAACTCACGGGCCCGAGGGGCTGCTTCAGGTCCTCCCGGAAGACTTTTG 360
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 TAATG-CGTATAAACGTAAGTACTTAAATGACTAGGAGTGGTTCTTGAGACCGATGAGAG 179
BnFAE1 CGGCGGCGCGTGAAGAGACGGAGC-AAGTTATCATTGGTGCGCTAGAAAATCTATTCAAG 419
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 A----TGGGAGCAGAACTAAAGATGATGACATAATTAAGAACGAATTTGAAAGGCTCTTA 235
BnFAE1 AACACCAACGTTAACCTTAAGATATAGGTATACTTGTGG-TGAACCTAAGCATGTTTAA 478
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 GGT TTGAATCCTATTTCGAGAATGTTTTTGTCAAAGATAGTGGCGA-ITTTGAACCAAAGA 294
BnFAE1 ---TCCAACCTCCATCGCTCTCCCGATGGTTCGTTAACACTTTTCAAGCTCCGAAGCAACGT 535
  *  **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 AAACATTTAAAAAATCAGTATCC--GGTTAC-GTTCATGCAA-ATAGAAAGTGGTCTAGG 350
BnFAE1 AAGAAGCTTTAACCTTGGTGGCATGSGTTGTAGTGCCSGCGTTATAGCCATTGATCTAGC 595
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 ATCTGATTGTAATTTTAGACTTAAAGAGTCTCTTAAGATTCAATCCTGGCTGTGTACAAA 410
BnFAE1 AAAGGACTT--GTTGCATGTCCATAAAAATACGTATGCTCTTGTGGTGAGCACAGAGAAC 653
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 ACTACAAATAATATAT---TTTAGACTATTTGGCCTTAACATAACTTCCACTCATTATTT 467
BnFAE1 ATCACTTATAACATTTACGCTGGTGATAATAGGTCCATGATGGTTTCAAATTGCTTGTTC 713
  *  **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 ACTGAGGTTAGAGA-ATAGACTTGCGAATAAACACATTCCCGAGAAATACTCATGATCCC 526
BnFAE1 CGTGTGGTGGGGCCGCTATTTTGTCTCCAAACAAG--CCTGGAGATCGTAGACGGTCCA 771
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 -----CE3-----
BnFAE1 ATAATTAGTCAGAGGGTATG--CCAATCAGATCTAAGAACACACATTCCCTCAAAATTTTA 584
  AGTACGAGCTAGTTACACGGTTTCGAACGCATACCGGAGCTGACGACAAGTCTTTTCGTT 831
  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *

AtFAE1 ATGCACATGTAATCATAGTTTAGCACAATTCAAAAATAATGTAGTATTAAAGACAGAAAT 644
BnFAE1 GCGTGCAACAAGGAGACGATGAGAACGGCAAAATCGGAGTGAGTTTGTCCAAGGACATAA 891
  *  **  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *  *
  
```

FIG. 8A



15/15

ALIGNMENT OF *B.n.* AND *A.t.* *FAE1* PROMOTERS (CONTINUED)

```
AtFAE1 TTGTAGACTTTTTTTTGGCGTTAAAGGAAGACTAAG-----TTTATACGTACATTTTAT 698
BnFAE1 CCGATGTTGCTGGTTCGAACGGTTAAGAAAAACATAGCAACGTTGGGTCCGTTGATTCTTC 951
      * * * * * * * * * * * * * * * * * * * * * * * * * * * *

AtFAE1 T-TTAAGTGGAAAACCGAAATTTTCCAT-----CGAAATATATGAATTTAGTATATATA 751
BnFAE1 CGTTAAGCGAGAAACTTCTTTTTCGTTACCTTCATGGGCAAGAACTTTTCAAAGATA 1011
      * * * * * * * * * * * * * * * * * * * * * * * * * * * *

                        G box 2
AtFAE1 TTTCTGCAATGTACTATTTTGGCTATTTTGGCAACTTTTCAGTGGACTACTACTTTAT-TAC 810
BnFAE1 AAATCAAACATTACTACGTCCCGGATTTC-AACCTTGCTATTGACCATTTTGTATACAT 1070
      * * * * * * * * * * * * * * * * * * * * * * * * * * * *

                        G-box 1
AtFAE1 AATGTGTATGGATGCATGAGTT-TGAGTATACACATGCTCTAAATGCATGCTTTGCAAAAC 869
BnFAE1 GCCGGAGGCAGAGCCGTGATTGATGTCTAGAGAAGAACCTAGCCCTAGCACCGATCGAT 1130
      * * * * * * * * * * * * * * * * * * * * * * * * * * * *

AtFAE1 GTAACGG-ACCACAAAAGAGGATCCAT-----GCAAATACATCTCATAGCTTCCTCCAT 922
BnFAE1 GTAGAGGCATCAAGATCAACGTTACATAGATTGGAAACACTTCATCTAGCTCAATATGG 1190
      * * * * * * * * * * * * * * * * * * * * * * * * * * * *

AtFAE1 TATTTTCCGACACAAACAGA-GCA----- 945
BnFAE1 TATGAGTTGGCATACATAGAAGCAAAGGAAGGATGAAGAAAGGTAAATAAGTTTGGCAG 1250
      * * * * * * * * * * * * * * * * * * * * * * * * * * * *

AtFAE1 -----
BnFAE1 ATTGCTTTAGGGTCAGGCTTTAAGTGTAACAGTGCAGTTTGGGTGGCTCTAAACAATGTC 1310

AtFAE1 -----
BnFAE1 AAAGCTTCGACAAATAGTCCTTGGGAACACTGCATCGACAGATACCCGGTCAAAATTGAT 1370

AtFAE1 -----
BnFAE1 TCTGATTCAGGTAAGTCAGAGACTCGTGTCCAAAACGGTCGGTCCTAATAAACGATGTTT 1430

AtFAE1 -----
BnFAE1 GCTCTCTTTCGTTTCTTTTATTGTTATAATAATTTGATGGCTACGATGTTTCTCTTGT 1490

AtFAE1 -----
BnFAE1 TTGTTATGAATAAAGAATGCAATGGTGTTCTAGTATTTGATTGTTTTACATGTATGTATC 1550

AtFAE1 -----
BnFAE1 TCTTATTACATGAAATTTTTAAACGCCTAAAAAACAACGGAATTCCG 1600
```

FIG. 8B